REMARKS

I. Telephonic Interview Summary

On August 8, 2006, Applicants' Representative and the Examiner discussed the present restriction requirement in a telephonic interview. Applicants thank the Examiner for clarifying the restriction requirement and explain below why the claimed nucleic acids, or respectively the polypeptides, are members of a single genus of invention and do not constitute independent and patentably distinct inventions requiring election of a single nucleic acid, or respectively a polypeptide, for prosecution.

II. Status of the Claims

With this response, claims 17-19, 22, 23, 26, 30, 38, 39, 41, 49, and 50 are amended; claims 20, 21, 24, 25, 27-29, 33-37, 43-48, and 71 are canceled; claims 1-16, 51-70, and 72-86 are withdrawn as being directed to non-elected groups; and new claims 87-96 are added. The amendments presented herein do not add new matter. They are made solely to revise claim dependency, improve claim terminology, and/or clarify the invention. Support for all amendments are present in the Sequence Listing, Drawings, and Specification as detailed herein.

Specifically, claim 17 is amended to improve its reading, the consistency of the terminology, and to clarify the meaning of the claimed polypeptides. Specific support for the amendment can be found in the specification at p. 7, lines 3-4, 18-23; p. 29, lines 18-21; p. 30, lines 4-10; p. 31, lines 6-9, 18-22; p. 33, lines 4-13; p. 34, lines 7-17; p. 35, lines 4-8; and p. 36, lines 5-9.

Claim 18 is amended to better define the invention of claim 17. Support for claim 18 is found in the specification at p. 10, lines 1-4; p.38, lines 17-21; and p. 43, lines 9-13.

Claim 19 and 41 are amended to improve the consistency of the claims' terminology.

Claim 22 and 26 are amended to depend from claim 17, improve the consistency of their terminology, and clarify the claimed polypeptides. Support for the amendment is found in the Specification at p. 31, lines 14-21 and p. 34, lines 7-10.

Claim 23 is amended to clarify the claimed polypeptides.

Claim 30 is amended to include the limitations previously presented in dependent claims 33-37.

Claims 38 and 39 are amended to correct claim dependency and clarify the meaning of the identified sequences. Support for the amendment is found in the Specfication at p. 17, lines 21-23, p. 31, line 22; and p. 34, lines 7-8 and 22-23.

Claim 49 is amended to better identify the claimed polypeptides. Support for the amendment is found throughout the Specification, in particular at p. 30, line 13 to p. 31, line 5.

Claim 50 is amended to depend from Claim 19.

New claim 87 is added to further define the invention of claim 17; new claims 88-90 are added to further define the invention of claim 26; new claims 91-93 are added to further define the invention of claim 30; and new claims 94-96 are added to further define the invention of claim 49. Support for the new claims is found at p. 8, lines 21-23; p. 10, lines 1-4; p. 16, lines 16-18; p. 43, lines 9-10; and original claims 18 and 19.

With the amendments and election of Invention II original claims 31, 32, 40, and 42; amended claims 17-19, 22, 23, 26, 30, 38-39, 41, 49, and 50; and new claims 87-96 are asserted to be in the case and ready for examination.

III. Applicants Invention

Activation of caspase leads to apoptosis, a process that is disrupted by hyperproliferative diseases. Applicants' invention relates to methods and compositions for cleaving IAP and, thereby, promoting caspase activation, as well as, methods and compositions for inhibiting cleavage of IAP and caspase activation. Applicants claim mutant Omi polypeptides and fragments of Omi proteins that are useful for either promoting or preventing apoptosis and studying hyperproliferative diseases.

IV. Restriction to a Single Sequence Is Improper as the Sequences Are Closely Related and No Serious Burden Exists

35 U.S.C. §121 provides that restriction is proper if there are two or more independent and distinct inventions presented in an application. Nevertheless, "[i]f the search and examination of all the claims in an application can be made without serious burden, the examiner *must examine them on the merits*, even though they include claims to independent or distinct inventions." MPEP § 803 (emphasis added). And, "[i]f the members of the Markush group are sufficiently few in number or so closely related that a search and examination of the entire claim can be made without serious burden, the examiner *must examine all the members of the Markush group in the claim on the merits*, even though they may be directed to independent and distinct inventions." MPEP § 803.02 (emphasis added).

In this case, restriction is not proper because the sequences-at-issue are sufficiently closely related to each other that a search and examination of the entire claim can be made without serious burden.

A. Nucleic acid sequences, SEQ ID NOs: 2-41, represent a single genus of invention

Herein, for the purposes of establishing that SEQ ID NOs. 2-41 represent a single genus of invention, the sequences are discussed as they relate to the wild type Omi nucleotide sequence (SEQ ID NO. 1).

SEQ ID NOs. 2-5 are full length mutants of wild type Omi polypeptide (SEQ ID NO. 1). SEQ ID NOs. 2 and 3 contain point mutations at positions 193, 195, 285, and 519 (see Table 1). SEQ ID NO. 4 contains an additional point mutation at position 284, and SEQ ID NO. 5 contains the aforementioned five point mutations plus mutations at positions 283, 284, 517, and 518.

SEQ ID NOs. 6-41 are fragments of SEQ ID NO. 1 as summarized in Table 1. SEQ ID NOs. 6, 11, 14, 17, 22, 25, 34, 40, and 41 lack any mutations. SEQ ID NOs. 7-8, 12-13, 15-16, 18-19, 23-24, and 26-27 contain point mutations at positions 193, 195, 285, and 519. SEQ ID NOs. 4, 9, 20, and 28 contain the aforenamed point mutations plus an additional mutation at position 284 for a total of five point mutations. SEQ ID NOs. 10, 21, and 29 each contain point mutations at positions 193-195, 283-285, and 517-519. SEQ ID NOs. 30-33, and 35-39 contain point mutations at positions 193, 195, 285, and 519, as well as, deletions at positions 160-162, 229-231, 370-372, or 530-532, respectively.

Table 1. Claimed nucleotide sequences and their relationship to SEQ ID NO: 1.

SEQ ID NO.	positions relative to SEQ ID NO. 1	Variation from SEQ ID NO. 1 (positions relative to SEQ ID NO. 1)	Support in specification[1]
2-3	1-975	Substitutions at 193, 195, 285, 519	p. 19, ln 4-5, 14-20
4	1-975	Substitutions at 194, 195, 284, 285, 519	p. 19, ln 4-5, 14-20
5	1-975	Substitutions at 193-195, 283-285, 517-519	p. 19, ln 4-5, 16-20
6	1-675	None	p. 20, ln 10-11, 16-19
7-8	1-675	Substitutions at 193, 195, 285, 519	p. 20, ln 10-12, 16-19

SEQ ID NO.	positions relative to SEQ ID NO. 1	Variation from SEQ ID NO. 1 (positions relative to SEQ ID NO. 1)	Support in specification[1]
9	1-675	Substitutions at 194, 195, 284, 285, 519	p. 20, ln 10-12, 16-20
10	1-675	Substitutions at 193-195, 283-285, 517-519	p. 20, ln 10-12, 16-20
11	13-975	None	p. 21, ln 6
12-13	13-975	Substitutions at 193, 195, 285, 519	p. 21, ln 6-7
14	13-675	None	p. 20, ln 16-19; p. 21, ln 12-14
15-16	13-675	Substitutions at 193, 195, 285, 519	p. 21, ln 12-16
17	1-636	None	p. 20, ln 16-19; p. 21, ln 20-22
18-19	1-636	Substitutions at 193, 195, 285, 519	p. 21, ln 20-22; p. 22, ln 1-2
20	1-636	Substitutions at 194, 195, 284, 285, 519	p. 21, ln 20-22; p. 22, ln 1-2
21	1-636	Substitutions at 193-195, 283-285, 517-519	p. 21, ln 20-22; p. 22, ln 1-2
22	13-636	None	p. 22, 3-6
23-24	13-636	Substitutions at 193, 195, 285, 519	p. 22, ln 3-9
25	1-630	None	p. 22, ln 4, 15-16
26-27	1-630	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 11-12, 17-18
28	1-630	Substitutions at 194, 195, 284, 285, 519	p. 22, ln 4, 11-12, 17-18
29	1-630	Substitutions at 193-195, 283-285, 517-519	p. 22, ln 4, 11-12, 17-18
30	1-159; 163-636	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 19-21
31	1-228; 232-636	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 19-21
32	1-369; 373-636	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 19-21
33	1-529;	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 19-21

SEQ ID NO.	positions relative to SEQ ID NO. 1	Variation from SEQ ID NO. 1 (positions relative to SEQ ID NO. 1)	Support in specification[1]
	533-636		
34	13-630	None	p. 22, ln 4, 21-22
35	13-630	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 21-23
36	13-159; 163-636	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 21-23
37	13-228; 232-636	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 21-23
38	13-369; 373-636	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 21-23
39	13-529; 533-636	Substitutions at 193, 195, 285, 519	p. 22, ln 4, 21-23
40	676-975	None	p. 20, ln 8
41	1-12	None	p. 17, ln 22; p. 21, ln 1-2

[1]Support is found in the Sequence Listing and as noted.

The greatest variation between SEQ ID NO. 2 and any of SEQ ID NOs. 3-41 is less than 2% (compare, for example, SEQ ID NO. 29 which contains nine point mutations in a 630 base segment of SEQ ID NO. 2). Clearly, SEQ ID NO. 2 shares a core sequence with SEQ ID NOs. 3-41, and any search for sequences homologous to SEQ ID NO. 2 will inevitably also search for any sequences homologous to SEQ ID NOs. 3-41. Thus, no serious search burden is presented by SEQ ID NOs. 3-41.

In light of the foregoing remarks, Applicants assert that the restriction to a single nucleotide sequence is improper and SEQ ID NOs. 2-41 must be examined together on their merits. *See* MPEP §§ 803, 803.02. Applicants request withdrawl of the restriction to a single sequence.

B. Polypeptide sequences, SEQ ID NOs. 45-77 represent a single genus of invention

For the purposes of establishing that SEQ ID NOs. 45-77 represent a single genus of inveniton, the sequences are discussed herein as they relate to SEQ ID NO. 44, which represents the 325 amino acid, wild type, mature Omi polypeptide.

SEQ ID NOs. 45-47 are full length mutants of wild type Omi polypeptide (SEQ ID NO. 44) that contain mutations at positions 65, 95, and 173 (see Table 2). SEQ ID NOs. 48-77 are fragments of SEQ ID NO. 44 that do or do not contain mutations as described below.

SEQ ID NOs. 48, 52, 54, 56, 60, 62, 70, 76, and 77 lack mutation. SEQ ID NOs. 49-51, 53, 55, 57-59, 61, 63-65, and 71 contain mutations at positions 65, 95, and 173. SEQ ID NOs. 66-69 and 72-75 are fragments that contain the same three mutations, as well as, a single residue deletion at position 54, 77, 124, or 177, respectively.

Table 2. Claimed polypeptide sequences and their relationship to SEQ ID NO: 44.

SEQ ID NO.	positions relative to SEQ ID NO. 44	Variation from SEQ ID NO. 44 (positions relative to SEQ ID NO. 44)	Support in specification[1]
45-47	1-325	Substitutions at 65, 95, 173	p. 30, ln 9-12
48	1-225	None	p. 31, ln 18-22; p. 32, ln 15-16
49-51	1-225	Substitutions at 65, 95, 173	p. 31, ln 18-21; p. 32, ln 16-19
52	5-325	None	p. 34, ln 10-16
53	5-325	Substitutions at 65, 95, 173	p. 34, ln 10-16
54	5-225	None	p. 33, ln 10-11; p. 34, ln 14-17
55	5-225	Substitutions at 65, 95, 173	p. 33, ln 12-13; p. 34, ln 14-17
56	1-212	None	p. 33, ln 16-18
57-59	1-212	Substitutions at 65, 95, 173	p. 33, ln 16-19
60	5-212	None	p. 33, ln 20-22
61	5-212	Substitutions at 65, 95, 173	p. 33, ln 22 – p. 34, ln 1

SEQ ID NO.	positions relative to SEQ ID NO. 44	Variation from SEQ ID NO. 44 (positions relative to SEQ ID NO. 44)	Support in specification[1]
62	1-210	None	p. 34, ln 1-2
63-65	1-210	Substitutions at 65, 95, 173	p. 34, ln 1-5
66	1-53; 55-212	Substitutions at 65, 95, 173	p. 34, ln 3-5
67	1-76; 78-212	Substitutions at 65, 95, 173	p. 34, ln 3-5
68	1-123; 125-212	Substitutions at 65, 95, 173	p. 34, ln 3-5
69	1-176; 178-212	Substitutions at 65, 95, 173	p. 34, ln 3-5
70	5-210	None	p. 34, ln 5-6
71	5-210	Substitutions at 65, 95, 173	p. 34, ln 3-6
72	5-53; 55-212	Substitutions at 65, 95, 173	p. 34, ln 3-6
73	5-76; 78-212	Substitutions at 65, 95, 173	p. 34, ln 3-6
74	5-123; 125-212	Substitutions at 65, 95, 173	p. 34, ln 3-6
75	5-176; 178-212	Substitutions at 65, 95, 173	p. 34, ln 3-6
76	226-325	None	p. 31, ln 22
77	1-4	None	p. 34, ln 7-8

[1]Support is found in the Sequence Listing and as noted.

The greatest variation between SEQ ID NO. 45 and any of the SEQ ID NOs. 46-77 is less than 2%. Clearly, SEQ ID NO. 45 and SEQ ID NOs. 46-77 share a core sequence, and any search for sequences homologous to SEQ ID NO. 45 will necessarily also search for any sequences homologous to SEQ ID NOs. 46-77. Thus, no serious search burden is presented by SEQ ID NOs. 46-77.

In light of the foregoing remarks, Applicants assert that the restriction to a single polypeptide sequence is improper and SEQ ID NOs. 45-77 must be examined together on their merits. *See* MPEP §§ 803, 803.02. Applicants request withdrawl of the restriction to a single sequence.

V. Conclusion

Applicants request that the foregoing amendments and remarks be entered and considered. Specifically, Applicants request that the restriction to a single sequence be withdrawn, and new claims 87-96 be entered and considered as part of Invention II. Should the Examiner have any question or comment as to the form, content, or entry of this Amendment and Response, the Examiner is requested to contact the undersigned at the telephone number below.

Respectfully submitted,

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